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Result
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Listing first 45 summaries
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Q13577
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4 molluscum c
5 homo sapien
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6 brassica na
8 rarbidopse
8 felis silve
1 pseudorabie
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SEQUENCE OF 205-240 FROM N.A.

MEDLINE=91267564; PubMed=1711009; vochikawa K., Seto M., Ueda R., Obata Y., Notake K.,

Yokochi T.,

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333
                                             EMBL; X06180; CAA29546.1; -.
EMBL; M37271; AAA51953.1; -.
EMBL; BC009293; AAH09293.1; -.
EMBL; BC013297; AAH13297.1; -.
EMBL; D00749; BAA00646.1; JOINED
EMBL; D00747; BAA00646.1; JOINED
EMBL; D00748; BAA00646.1; JOINED
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EMBL; A39016; A39016.
                                                                                                                                                                                                                                                     GO; GO:0016021; C:integ
GO; GO:0005624; C:memb;
GO; GO:0005886; C:plasm;
GO; GO:0004872; F:recep
GO; GO:0004872; F:recep
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J. Biol. Chem. 275:3431-3437(2000).

J. Biol. Chem. 275:3431-3437(2000).

I. FUNCTION: Not yet known.

I. SUBUNIT: Interacts with SECTM1.

I. SUBURITAR LOCATION: Type I membrane protein.

I. SIMILARITY: Contains I immunoglobulin-like domain.

I. DATABASE: NAME=PROW; NOTE=CD guide CD7 entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd7.htm".
                                                                                                      SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01607; 1BWW.
Genew; HGNC:1695; CD7.
H-InvDB; HIX0014252; -.
                                                                                                                                                                                                               InterPro; IPR007110; Ig-like. Pfam; PF00047; ig; 1. SMART; SMONAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20119303; PubMed=10652336; DOI=10.1074/jbc.275.5.3431; Lyman S.D., Escobar S., Rousseau A.-M., Armstrong A., Fanslow W.C.; "Identification of CD7 as a cognate of the human K12 (SECTM1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of the surface topography structure of the human CD7 molecule.";
                                               DOMAIN
                                                                                                                                                                Antigen; Glycoprotein; Immune response; Immunoglobulin do
Lipoprotein; Palmitate; Receptor; Repeat; Signal; T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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Ware R.E., Scearce R.M., Dietz M.A.,
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Takahashi T.;
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immunogenetics 33:352-360(1991).
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                                                                                                                                                                                                                                                                 GO:0016021; C:integral to membrane; TAS.
GO:0016021; C:membrane fraction; TAS.
GO:0005624; C:membrane fraction; TAS.
GO:0005886; C:plasma membrane; TAS.
GO:0004872; F:receptor activity; TAS.
GO:0004872; F:receptor activity; TAS.
GO:00042110; P:T-cell activation; TAS.
GO:0007169; P:transmembrane receptor protein tyrosine kin. . .;
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Potential
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                                                                                                                                                                                                           Hypothetical protein.
OrderedLocusNames=SAV5394;
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01-OCT-2003
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MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzad
Smith D.F.;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein L3302.06.
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Q9N9M7;
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Quail M., Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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      STRAIN=MA-4680;
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                                                                                                                                                 Bacteria;
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N-linked (GlcNAc. . .
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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NCBI_TaxID=7227
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Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005042; BAC73106.1; -.
GO; GO:0016020; C:membrane; IEA.
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945DD9B79E75AAE2 CRC64;
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whittfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                Submitted (MAR-2004) to the EMBL; AE003492; AAF48251.1; Intact; Q9VYE7; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
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MEDLINE=22426070; PubMed=12537573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287:2185-2195 (2000).
                                                            SALPAPPT--GSALPDPQTASALPDPPAAS--ALPAALAV-ISFLLGLGLGVACVLART
                                                                                                                                                                                                                                                                          FBgn0030470; CG12724.
SAATATPTASGSATPTPSPTS--PNPPAVGGMGLPMPLTLGLGLGLGLGMGMGVVSRLRRT
                                                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 review.
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3:RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milshina N.V., Mobarry C.,
                                                                                                                                                                                                                                              Α,
                                                                                                                                                     29.0%;
                                                                                                                                                                                                                                              14524 MW;
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                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                     Score 83.5;
Pred. No. 6
                                                                                                                                                                                                                                              12E97DA73AFA8319 CRC64;
                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B., Carlson J., S
S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morris J.,
                                                                                                                                                     8
                                                                                                                                                                                    BB
                                                                                                                        21;
                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                 Length 145;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moshrefi A.,
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   89
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RESULT Q6PCS2

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WA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Branstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nitlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Marty M. M. A., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,

A Jones S. T. Mayra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Toyyrinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6PCS2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein zgc:64189.
ORFNames=zgc:64189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                      Q9VYF9
Q9VYF9;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-2003) to the EMBL/GenB
EMBL; BC059189; AAH59189.1; -
ZFIN; ZDB-GENE-040426-1397; ZGC:64189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
STRAIN=Berkeley;
Stapleton M., Brokstein P.,
                                                               Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                       ORFNames=CG12723;
                                                                                                                                                                                       01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                           358
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                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                     ALPAPPTGSALPDPQTASALPDPPAASALPA 35
                                                                                                                                                                                                                                                                                                                                           ALPAPPKULALPAPPRULALPAPPRULALPA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 protein.
                                                                                                                                                                                     (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acad.
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27,
                                                                                                                                                                                       13,
24,
24,
                                                                                                                                                                                                                                                                                                                                                                                                          Score 83; DB Pred. No. 30; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
   Hong L., Agbayani A., Carlson
                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72E3F6955AFB95B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 690;
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RAPA BERARA BERA
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RA Adams M.D., Celniker S.E., Holt R.A., EVANS C.A., Golayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt R.A., EVANS C.A., Golayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt R.A., EVANS C.A., Golayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.K.,
RA Barndon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D.,
RA Ballew R.M., Doyle C., Baxter B.G., Helt G., Welson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Broketein P., Borttier P.,
RA Borkova D., Botchan M.R., Bouck J., Broketein P., Borttier R.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Broketein P., Bortier S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Carrey D., Heiman T.J., Mays S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Liai Z.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lin X.,
Ra Kimmel B.E., Kodira C.D., Kodend M., Lin K.,
Ra Kimmel R., Mayshy B., Murphy L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7Z2C5
Q7Z2C5;
Q1-OCT-2003
Q1-OCT-2003
Q1-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Champe M., Chavez C., Dorsett V., Dresnek D., George R., Gonzalez M., Guarin H., Kronmiller Miranda A., Mungall C.J., Nunoo J., Pacleb J., Patel S., Phouanenavong S., Wan K., Yu C., Lew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY119125; AAM50985.1; -.
PlyBase; FBgn0030459; CG12723.
SEQUENCE 553 AA; 58356 MW; OFF2A5A1C6512B88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orespanica melanogaster (Fruit 11y).
Drosophila melanogaster (Fruit 11y).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=CG12723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 82; DB 2
Pred. No. 30;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Dresnek D., Farfan D., Fris
., Kronmiller B., Li P., Liao
J., Pacleb J., Paragas V., Pa
K., Yu C., Lewis S.E., Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           625
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                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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  MEDLINE=96079124;
Hejna J.A., Saito
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Ashburner M., Celniker S.E.;
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                                                                                                                             Catarrhini;
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RX MEDILINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Berandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J. Bayraktarogli L., Beasley E.M., RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottier P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hermandez J.R., Houck J., Hortland T.J., Hermandez J.R., Houck J., Andervitz S., Kulp D., Lai Z., Lake P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Alake P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulow G., Milshina N.V., Mobarry C., Morris J., Mosheria A., Ra Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H., Ra Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H., Ra Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H., Ra Rainert K., Rassarman D.A., Weinstook G.M., Weissenbach J., Mang X., Wan B., Woodaget, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Ra Williams S.M., Woodaget, Worley K.C., Mu D., Zhao Q., Zheng L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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OR GO: 0045254; C: pyruvate dehydrogenase complex; IEA.

RGO; GO:0008415; F: acyltransferase activity; IEA.

RGO; GO:0004742; F: dihydrolipyllysine-residue acetyltransfera. . .; IEA.

RGO; GO:0005515; F: protein binding; IEA.

RGO; GO:0005515; F: protein binding; IEA.

RGO; GO:0006740; F: transferase activity; IEA.

RGO; GO:0006096; P: glycollysis; IEA.

RGO; GO:0006096; P: metabolism; IEA.

RGO; GO:0008152; 
                       Query Match
Best Local (
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase full SIMILARITY: Contains 1 lipoyl-binding domain.

EMBL, AE003617; AAF52515.1; -.

HSSP, P11961; 1B5S.
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Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MADLINE=22426070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller Patel S., Frise B., Wheeler D.A., Lewis Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     systematic review."
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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                                                                                                             PROSITE; PS00189; LIPOYL; I.
ACYltransferase; Lipoyl; Transferase
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  Mismatches
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S.E.,
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                                             Length 421;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Maril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakearoglu L., Beasley E.M.,
RA Ballew R.M., Beau A., Baxendale J., Bayrakearoglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahle C., Davaport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dayra R., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J. Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lais Y., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lais Y., Lai Y., Lai Y., Lai Y., Lai Z., Liang Y., Lii X.,
RA Welson D.R., Nelson K.A., Naxon K., Nusskern D.R., Pacleb J.M.,
RA Kimmel B.E., Kodira C.D., Fara K., Wunter J., San A.H., Wang X.
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchtromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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01-MAY-2000 (TrEMBLrel.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pfam; PF00364; Biotin lipoyl; 1.
Pfam; PF002817; B3 binding; 1.
ProDom; PD001115; 20xoacid dh; 1.
TIGREAMS; TIGR01349; DDHac trf mito; 1.
PROSITE; PS00189; LIPOYL; I.
ACYLTransferase, Lipoyl; Transferase.
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR006257; AceFtransferaseL.
InterPro; IPR006257; AceFtranipy1.
InterPro; IPR004167; E3 binding.
InterPro; IPR011053; Hybrid_motif.
InterPro; IPR003016; Lipoyl_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P10515; 1FYC. IntAct; Q9VM14; - FlyBase; FBgn003191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Kaminker J.S., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
                                        Q6FTP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                   Base; FBgn031912; CG5261.
GG:0045254; C:pyruvate dehydrogenase complex; IEA.
GG:0004515; F:acyltransferase activity; IEA.
GG:0004742; F:dihydrolipoyllysine-residue acetyltransfera..
GG:0004742; F:protein binding; IEA.
GG:0005515; F:protein binding; IEA.
GG:0005516; F:transferase activity; IEA.
GG:000695; F:glycolysis; IEA.
GG:00069152; P:metabolism; IEA.
                                                                                                            173
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                                                                                                                                                                              Similarity
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                                                                                                                                    ASALPAPPTGSALPDPQTASALPDPPAASALPAALA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               review.
(TrEMBLrel.
                                         PRELIMINARY;
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 Last sequence update)
                                                                                                                                                                              Score 81;
Pred. No.
                                         PRT;
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Best Local S
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  Query Match
Best Local S
Matches 19
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A Lafontaine I. de Montigny J., Marck C., Neuveglise C., Talla E.,
A Lafontaine I. de Montigny J., Marck C., Neuveglise C., Talla E.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet F., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropulos O.,
Pellenz S., Potter S., Richard G.F., Ozier-Kalogeropulos D.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                       Ohsawa K., Black D.H., Sato H., Rogers K., Ebe:
"Sequence and genetic arrangement of the UI re;
virus (Cercopithecine herpesvirus 1) genome and
region of other primate herpesviruses.";
Arch. Virol. 148:989-997(2003).
EMBL; AB096160; BACS8076.2;
InterPro; IPR00528; Herpes teg_N.
InterPro; IPR005210; Herpes U136.
Pfam; PF04843; Herpes U136.
Pfam; PF04843; Herpes U136; 1.
SEQUENCE 3326 AA; 345566 MW; 6B53E3B60F43C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecine herpesvirus 1 (CeHV-1)
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
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01-MAR-2004 (TrEMBLrel.
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01-0CT-2003
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MEDLINE=22607624; PubMed=12721804;
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Bukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similar to sp|P37370 Saccharomyces cerevisiae YLR337c VRP1. ORFNames=CAGL0G00968g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00246; WH2;
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Last annotation update)
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Score 81; DB 2;
Pred. No. 1.8e+02
0; Mismatches 1
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                                                                                                                   6B53E3860F43CDF0 CRC64;
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Herpesviridae;
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                                                                                                                                                                                                                                                                                                                                           region of the monkey and comparison with
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QSYDH2

ID QSYDH

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AC CATYT

AC STRALL

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RX ESDILL

RX CAMPDLL

RX CAMPDL
Q7YXK4
Q7YXK4
ID Q7YXK
AC Q7YXK
AC Q7YXK
AC Q7YXK
AC Q7YXK
D7 01-00
D7 01-01
D8 MFP1
OS Ascan
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Matches 20
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Q7YXK4;
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Q1-NOV-1999 (TrEMBLrel. 12,
Q1-NOV-1999 (TrEMBLrel. 12,
Q1-MAR-2004 (TrEMBLrel. 26,
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Microbiology 145:3487-3495(1999).

EMBL; AF071081; AAD41594.1; -.

GO; GO:0005199; F:structural constituent of cell wall; IEA.
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InterPro; IPR003882; Pistil extensin.
PRINTS; PR01222; ATROPHIN.
PRINTS; PR01218; PSTLEXTENSIN.
SEQUENCE 763 AA; 75034 MW; 39168F
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                                       similarity).
-!- SIMILARITY: Contains 1 MSP domain.
-!- SIMILARITY: Contains 1 MSP domain.
EMBL; AY326285; AAP94884.1; -.
GO; GO:0005856; C:cytoskeleton; IEA.
GO; GO:0005198; F:structural molecule
                                                                                                                                                                                                                                                                                                                                            MEDLINE=23001057; PubMed=14565983;
Buttery S.M., Ekman G.C., Seavy N., Stewart M., Roberts T.M.;
"Dissection of the Ascaris sperm motility machinery identifies key proteins involved in major sperm protein-based amoeboid locomotion.";
Mol. Biol. Cell 14:5082-5088 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Ascarididae; Ascaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20090472; PubMed=10627046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ascaris suum (Pig roundworm)
Eukaryota; Metazoa; Nematoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Testis
           InterPro;
                                                                                                                                                                                                                                                                                                    FUNCTION: Central component in molecular interactions underlying
                                                                                                                                                                                                                             sperm crawling. Forms an extensive filament from sperm villipoda, along the leading edge
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RESULT 15
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Q98274;
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Pfam; PF00635; Motile Sperm; 1.
PROSITE; PS50202; MSP; 1.
Cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96325459; PubMed=8670425;
Senkevich T.G., Bugert J.J., Sisler J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molluscum contagiosum virus subtype 1
Viruses; dsDNA viruses, no RNA stage;
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Science 273:813-815(1996).
EMBL, U60315; AAC55235.1; -.
PIR; T30709; T30709.
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milarity 48.6%;
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